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PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Nielsen et al.

Confirmation No: 6089

Serial No.: 10/038,723

Group Art Unit: 1652

Filed: January 2, 2002

Examiner: To be assigned

For: Glucoamylase Variants

SUPPLEMENTAL PRELIMINARY AMENDMENT

Commissioner for Patents
Washington, DC 20231

Sir:

Before examination, please amend the above-identified application as follows:

IN THE CLAIMS:

Please cancel claims 29-140 without prejudice or disclaimer.

Please add new claims 141-252, as follows:

141. An isolated variant of a parent glucoamylase comprising a mutation at one or more of the following positions in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in a homologous glucoamylase having at least 80% homology with the amino acid sequence shown in SEQ ID NO:2:

1, 2, 3, 4, 5, 6, 7, 8, 9, 11, 10, 12, 13, 14, 15, 16, 17, 18, 19, 21, 22, 23, 24, 25, 26, 28, 29, 31, 32, 33, 34, 35, 40, 41, 42, 43, 44, 45, 46, 47, 49, 51, 53, 56, 58, 60, 61, 62, 73, 74, 75, 76, 77, 78, 79, 80, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 109, 110, 111, 113, 114, 115, 117, 118, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 234, 235, 237, 238, 239, 240, 242, 243, 244, 245, 287, 288, 289, 290, 291, 292, 294, 295, 296, 298, 299, 300, 301, 303, 304, 308, 311, 314, 315, 316, 318, 319, 334, 335, 336, 337, 338, 339, 340, 341, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 384, 388, 390, 394, 397, 398, 399, 402, 403, 404, 405, 406, 409, 412, 413, 414, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470.

142. The variant of claim 141, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

143. The variant of claim 141, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.

144. The variant of claim 141, wherein said variant comprises a mutation at position 1 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

145. The variant of claim 141, wherein said variant comprises a mutation at position 2 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

146. The variant of claim 141, wherein said variant comprises a mutation at position 3 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

147. The variant of claim 141, wherein said variant comprises a mutation at position 4 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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148. The variant of claim 141, wherein said variant comprises a mutation at position 5 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

149. The variant of claim 141, wherein said variant comprises a mutation at position 6 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

150. The variant of claim 141, wherein said variant comprises a mutation at position 7 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

151. The variant of claim 141, wherein said variant comprises a mutation at position 8 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

152. The variant of claim 141, wherein said variant comprises a mutation at position 9 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

153. The variant of claim 141, wherein said variant comprises a mutation at position 11 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

154. The variant of claim 141, wherein said variant comprises a mutation at position 10 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

155. The variant of claim 141, wherein said variant comprises a mutation at position 12 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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156. The variant of claim 141, wherein said variant comprises a mutation at position 13 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

157. The variant of claim 141, wherein said variant comprises a mutation at position 14 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

158. The variant of claim 141, wherein said variant comprises a mutation at position 15 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

159. The variant of claim 141, wherein said variant comprises a mutation at position 16 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

160. The variant of claim 141, wherein said variant comprises a mutation at position 17 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

161. The variant of claim 141, wherein said variant comprises a mutation at position 18 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

162. The variant of claim 141, wherein said variant comprises a mutation at position 19 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

163. The variant of claim 141, wherein said variant comprises a mutation at position 21 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

164. The variant of claim 141, wherein said variant comprises a mutation at position 22 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

165. The variant of claim 141, wherein said variant comprises a mutation at position 23 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

166. The variant of claim 141, wherein said variant comprises a mutation at position 24 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

167. The variant of claim 141, wherein said variant comprises a mutation at position 25 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

168. The variant of claim 141, wherein said variant comprises a mutation at position 26 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

169. The variant of claim 141, wherein said variant comprises a mutation at position 28 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

170. The variant of claim 141, wherein said variant comprises a mutation at position 29 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

171. The variant of claim 141, wherein said variant comprises a mutation at position 31 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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172. The variant of claim 141, wherein said variant comprises a mutation at position 32 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

173. The variant of claim 141, wherein said variant comprises a mutation at position 33 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

174. The variant of claim 141, wherein said variant comprises a mutation at position 34 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

175. The variant of claim 141, wherein said variant comprises a mutation at position 35 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

176. The variant of claim 141, wherein said variant comprises a mutation at position 40 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

177. The variant of claim 141, wherein said variant comprises a mutation at position 41 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

178. The variant of claim 141, wherein said variant comprises a mutation at position 42 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

179. The variant of claim 141, wherein said variant comprises a mutation at position 43 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

180. The variant of claim 141, wherein said variant comprises a mutation at position 44 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

181. The variant of claim 141, wherein said variant comprises a mutation at position 45 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

182. The variant of claim 141, wherein said variant comprises a mutation at position 46 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

183. The variant of claim 141, wherein said variant comprises a mutation at position 47 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

184. The variant of claim 141, wherein said variant comprises a mutation at position 49 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

185. The variant of claim 141, wherein said variant comprises a mutation at position 51 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

186. The variant of claim 141, wherein said variant comprises a mutation at position 53 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

187. The variant of claim 141, wherein said variant comprises a mutation at position 56 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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188. The variant of claim 141, wherein said variant comprises a mutation at position 58 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

189. The variant of claim 141, wherein said variant comprises a mutation at position 60 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

190. The variant of claim 141, wherein said variant comprises a mutation at position 61 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

191. The variant of claim 141, wherein said variant comprises a mutation at position 62 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

192. The variant of claim 141, wherein said variant comprises a mutation at position 73 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

193. The variant of claim 141, wherein said variant comprises a mutation at position 74 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

194. The variant of claim 141, wherein said variant comprises a mutation at position 75 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

195. The variant of claim 141, wherein said variant comprises a mutation at position 76 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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Cont 196. The variant of claim 141, wherein said variant comprises a mutation at position 77 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

197. The variant of claim 141, wherein said variant comprises a mutation at position 78 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

198. The variant of claim 141, wherein said variant comprises a mutation at position 79 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

199. The variant of claim 141, wherein said variant comprises a mutation at position 80 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

200. The variant of claim 141, wherein said variant comprises a mutation at position 93 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

201. The variant of claim 141, wherein said variant comprises a mutation at position 94 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

202. The variant of claim 141, wherein said variant comprises a mutation at position 95 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

203. The variant of claim 141, wherein said variant comprises a mutation at position 96 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

204. The variant of claim 141, wherein said variant comprises a mutation at position 97 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

205. The variant of claim 141, wherein said variant comprises a mutation at position 98 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

206. The variant of claim 141, wherein said variant comprises a mutation at position 99 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

207. The variant of claim 141, wherein said variant comprises a mutation at position 100 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

208. The variant of claim 141, wherein said variant comprises a mutation at position 101 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

209. The variant of claim 141, wherein said variant comprises a mutation at position 102 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

210. The variant of claim 141, wherein said variant comprises a mutation at position 103 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

211. The variant of claim 141, wherein said variant comprises a mutation at position 104 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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212. The variant of claim 141, wherein said variant comprises a mutation at position 105 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

213. The variant of claim 141, wherein said variant comprises a mutation at position 106 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

214. The variant of claim 141, wherein said variant comprises a mutation at position 107 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

215. The variant of claim 141, wherein said variant comprises a mutation at position 109 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

216. The variant of claim 141, wherein said variant comprises a mutation at position 110 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

217. The variant of claim 141, wherein said variant comprises a mutation at position 111 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

218. The variant of claim 141, wherein said variant comprises a mutation at position 113 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

219. The variant of claim 141, wherein said variant comprises a mutation at position 114 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

220. The variant of claim 141, wherein said variant comprises a mutation at position 115 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

221. The variant of claim 141, wherein said variant comprises a mutation at position 117 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

222. The variant of claim 141, wherein said variant comprises a mutation at position 118 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

223. The variant of claim 141, wherein said variant comprises a mutation at position 200 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

224. The variant of claim 141, wherein said variant comprises a mutation at position 201 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

225. The variant of claim 141, wherein said variant comprises a mutation at position 202 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

226. The variant of claim 141, wherein said variant comprises a mutation at position 203 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

227. The variant of claim 141, wherein said variant comprises a mutation at position 204 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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228. The variant of claim 141, wherein said variant comprises a mutation at position 205 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

229. The variant of claim 141, wherein said variant comprises a mutation at position 206 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

230. The variant of claim 141, wherein said variant comprises a mutation at position 207 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

231. The variant of claim 141, wherein said variant comprises a mutation at position 208 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

232. The variant of claim 141, wherein said variant comprises a mutation at position 209 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

233. The variant of claim 141, wherein said variant comprises a mutation at position 210 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

234. The variant of claim 141, wherein said variant comprises a mutation at position 211 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

235. The variant of claim 141, wherein said variant comprises a mutation at position 234 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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236. The variant of claim 141, wherein said variant comprises a mutation at position 235 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

237. The variant of claim 141, wherein said variant comprises a mutation at position 237 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

238. The variant of claim 141, wherein said variant comprises a mutation at position 238 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

239. The variant of claim 141, wherein said variant comprises a mutation at position 239 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

240. The variant of claim 141, wherein said variant comprises a mutation at position 240 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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242. The variant of claim 141, wherein said variant comprises a mutation at position 242 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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243. The variant of claim 141, wherein said variant comprises a mutation at position 243 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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244. The variant of claim 141, wherein said variant comprises a mutation at position 244 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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245. The variant of claim 141, wherein said variant comprises a mutation at position 245 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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246. The variant of claim 141, wherein said variant comprises a mutation at position 287 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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247. The variant of claim 141, wherein said variant comprises a mutation at position 288 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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~~248.~~ The variant of claim 141, wherein said variant comprises a mutation at position 289 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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~~249.~~ The variant of claim 141, wherein said variant comprises a mutation at position 290 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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~~250.~~ The variant of claim 141, wherein said variant comprises a mutation at position 291 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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~~251.~~ The variant of claim 141, wherein said variant comprises a mutation at position 292 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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~~252.~~ The variant of claim 141, wherein said variant comprises a mutation at position 294 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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~~253.~~ The variant of claim 141, wherein said variant comprises a mutation at position 295 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.